Amendments to Specification

Please replace the following paragraphs:

Paragraph beginning on page 12, line 10

SEQ ID NO:47 is the nucleotide sequence comprising the sugarbeet cDNA insert in clone ~~sugarbeet1~~sugarbeet2, encoding an almost entire sugarbeet isoflavone synthase.

Paragraph beginning on page 13, line 3

SEQ ID NO:60 is the ~~amino acid~~nucleotide sequence comprising the sugarbeet cDNA insert in clone ~~sugarbeet2~~sugarbeet1, encoding an almost entire sugarbeet isoflavone synthase.

Paragraph beginning on page 39, line 15

Amplification was carried out in two steps. The first amplification reaction was performed using 1 μL of first strand cDNA and primer set one (SEQ ID NO:11 and SEQ ID NO:12) with 30 cycles of 94°C for 30 seconds, 50°C for 30 seconds and 72°C for one minute. A second amplification reaction was done with 1 μL of the resulting product with primer set two (SEQ ID NO:13 and SEQ ID NO:14) and using 30 cycles of 94°C for 30 seconds, 50.5°C for 30 seconds and 72°C for one minute. The resulting PCR sequence was cloned into pCR2.1 using TOPO™ TA Cloning Kit (Invitrogen). Plasmid DNA was purified using QIAFilter cartridges (Qiagen Inc) or Wizard Plus Minipreps DNA Purification System (Promega) following the manufacturer's instructions. Sequence was generated on an ABI Automatic sequencer using dye terminator technology and using a combination of vector and insert-specific primers. Sequence editing was performed using DNAStar (DNASTAR, Inc.). All sequences represent coverage at least two times in both directions. The nucleotide sequence comprising the cDNA insert in clone ~~sugarbeet 1~~sugarbeet 2 is shown in SEQ ID NO:47; the deduced amino acid sequence of this DNA is shown in SEQ ID NO:48. The nucleotide sequence comprising the cDNA insert in clone ~~sugarbeet 2~~sugarbeet 1 is shown in SEQ ID NO:60[[61]]; the deduced amino acid sequence of this DNA is shown in SEQ ID NO:61.

Paragraph beginning on page 41, line 13:

A consensus sequence was determined by aligning the amino acid sequences of the present invention using the Clustal method of alignment and this sequence is shown in SEQ ID NO:66. Amino acids not conserved are indicated by Xaa. These are:

Xaa_{10}	Phe or Leu
Xaa_{16}	Ser or Leu
Xaa_{23}	Ser or Thr
Xaa_{25}	Ile or Lys
Xaa_{39}	Lys or Arg
Xaa_{48}	Pro or Leu
Xaa_{60}	Pro or Leu
Xaa_{73}	Leu or His
Xaa_{74}	Ser or Tyr
Xaa_{95}	Ala or Thr
Xaa_{96}	Asn or His
Xaa_{102}	Asn or Ser
Xaa_{110}	Ile, Val, or Thr
Xaa_{112}	Arg or His
Xaa_{117}	Asn or Ser
Xaa_{118}	Ser or Leu
Xaa_{121}	Met or Arg
Xaa_{122}	Ala or Val
Xaa_{124}	Phe or Ile
Xaa_{129}	Lys or Arg
Xaa_{147}	Lys or Glu
Xaa_{159}	Leu or Phe
Xaa_{162}	Ala or Val
Xaa_{166}	Ser or Gly
Xaa_{170}	Gln or Arg
Xaa_{175}	Val or Leu
Xaa_{183}	Ala or Thr
Xaa_{187}	Thr or Ile

3

Xaa$_{191}$ Met or Val

Xaa$_{209}$ Phe or Tyr

Xaa$_{219}$ Arg or Trp

Xaa$_{223}$ Tyr or His

Xaa$_{253}$ Gly or Glu

Xaa$_{259}$ Lys or Glu

Xaa$_{263}$ Val or Asp

Xaa$_{264}$ Val, Asp, or Ile

Xaa$_{268}$ Ala or Val

Xaa$_{272}$ Phe or Leu

Xaa$_{285}$ Thr or Met

~~Xaa$_{293}$ Glu or Asp~~

<u>Xaa$_{292}$ Any amino acid</u>

<u>Xaa$_{293}$ Any amino acid</u>

Xaa$_{294}$ Thr, or Ile

Xaa$_{301}$ Phe or Leu

Xaa$_{306}$ Thr or Ile

Xaa$_{311}$ Val or Glu

Xaa$_{312}$ Val or Ala

Xaa$_{325}$ Arg or Lys

Xaa$_{328}$ Gln or Glu

<u>Xaa$_{329}$ Any amino acid</u>

Xaa$_{334}$ Val or Ala

Xaa$_{342}$ Arg or Ile

Xaa$_{377}$ Thr or Ile

Xaa$_{381}$ Glu or Gly

Xaa$_{385}$ Tyr, His, or Cys

Xaa$_{387}$ Ile or Thr

Xaa$_{393}$ Val or Ile

Xaa$_{394}$ Leu or Pro

Xaa$_{402}$ Arg or Lys

Xaa$_{404}$ Ser or Pro

Xaa$_{413}$ Ser or Phe

4

Xaa$_{422}$ Glu or Gly

Xaa$_{428}$ Gly or Arg

Xaa$_{429}$ Pro or Leu

Xaa$_{435}$ Gln or Arg

Xaa$_{447}$ Arg or Gly

Xaa$_{453}$ Asn, Ser, or Ile

Xaa$_{459}$ Met or Thr, and

Xaa$_{485}$ Asp or Gly

Please replace the sequence listing with the enclosed amended sequence listing.